

**Amendments to the Claims:**

The following Listing of Claims will replace all prior versions, and listings, of the claims in the above-identified application.

**Listing of Claims**

1. (currently amended) An isolated and purified-poly(ADP-ribose) polymerase (PARP) homolog comprising human PARP2 (SEQ ID NO: 2) ~~or a functional equivalent thereof which is at least 95% homologous to~~ or a PARP homolog with at least 85% identity with human PARP2 (SEQ ID NO: 2), which exhibits poly(ADP-ribose)-synthesizing activity, and has an amino acid sequence which
  - a) has a functional NAD<sup>+</sup> binding domain comprising the sequence  
PX<sub>n</sub>(S/T)GX<sub>3</sub>GKGIYFA (SEQ ID NO:11)  
in which n is an integral value from 1 to 5, and the X radicals are, independently of one another, any amino acid;
  - and
  - b) lacks a zinc finger sequence of the formula  
CX<sub>2</sub>CX<sub>m</sub>HX<sub>2</sub>C (SEQ ID NO:30)  
in which m is an integral value of 28 or 30, and the X radicals are, independently of one another, any amino acid.
2. (previously presented) The PARP homolog as claimed in claim 1, wherein the functional NAD<sup>+</sup> binding domain comprises the following sequence:  
(S/T)XGLR(I/V)XPX<sub>n</sub>(S/T)GX<sub>3</sub>GKGIYFA (SEQ ID NO:12)  
in which n is an integral value from 1 to 5, and the X radicals are, independently of one another, any amino acid.
3. (currently amended) The PARP homolog as claimed in claim 1, ~~further~~ comprising the sequence:

LX<sub>9</sub>NX<sub>2</sub>YX<sub>2</sub>QLLX(D/E)X<sub>10/11</sub>WGRVG (SEQ ID NO: 15)

in which the X radicals are, independently of one another, any amino acid.

4-32. (canceled)

33. (previously presented) The PARP homolog as claimed in claim 1, wherein the functional NAD<sup>+</sup> binding domain comprises the following sequence:

LLWHG(S/T)X<sub>7</sub>IL(S/T)XGLR(I/V)XPX<sub>n</sub>(S/T)GX<sub>3</sub>GKGIYFAX<sub>3</sub>SKSAXY (SEQ ID NO:13)

in which n is an integral value from 1 to 5, and

the X radicals are, independently of one another, any amino acid.

34. (currently amended) The PARP homolog as claimed in claim 1, ~~further~~ comprising sequence:

AX<sub>3</sub>FXX<sub>4</sub>KTXNXWX<sub>5</sub>FX<sub>3</sub>PXK (SEQ ID NO:16)

in which the X radicals are, independently of one another, any amino acid.

35. (currently amended) The PARP homolog as claimed in claim 1, ~~further~~ comprising sequence:

XL(I/L)X<sub>2</sub>IX<sub>9</sub>MX<sub>10</sub>PLGKLX<sub>3</sub>QIX<sub>6</sub>L (SEQ ID NO:17)

in which the X radicals are, independently of one another, any amino acid.

36. (currently amended) The PARP homolog as claimed in claim 1, ~~further~~ comprising sequence:

FYTXIPHXFGX<sub>3</sub>PP (SEQ ID NO:18)

in which the X radicals are, independently of one another, any amino acid.

37. (currently amended) The PARP homolog as claimed in claim 1, ~~further~~ comprising sequence:

KX<sub>3</sub>LX<sub>2</sub>LXDIEXAX<sub>2</sub>L (SEQ ID NO:19)

in which the X radicals are, independently of one another, any amino acid.

38. (currently amended) An isolated poly(ADP-ribose) polymerase (PARP) homolog comprising human PARP2 (SEQ ID NO: 2) ~~or a functional equivalent thereof which is at least 95% homologous to~~ or a PARP homolog having at least 85% identity with human PARP2 (SEQ ID NO: 2), which exhibits poly(ADP-ribose)-synthesizing activity, and has an amino acid sequence which

- a) has a functional NAD<sup>+</sup> binding domain comprising the sequence

PX<sub>n</sub>(S/T)GX<sub>3</sub>GKGIYFA (SEQ ID NO:11)

in which n is an integral value from 1 to 5, and the X radicals are, independently of one another, any amino acid;

and

- b) lacks a zinc finger sequence of the formula

CX<sub>2</sub>CX<sub>m</sub>HX<sub>2</sub>C (SEQ ID NO:30)

in which m is an integral value of 28 or 30, and the X radicals are, independently of one another, any amino acid

further comprising a leucine zipper-like sequence:

(L/V)X<sub>6</sub>LX<sub>6</sub>LX<sub>6</sub>L (SEQ ID NO: 14)

wherein X radicals are, independently of one another, any amino acid.

39. (currently amended) The PARP homolog as claimed in claim 38, ~~further~~ comprising at least one of the following sequences:

LX<sub>9</sub>NX<sub>2</sub>YX<sub>2</sub>QLLX(D/E)X<sub>10/11</sub>WGRVG (SEQ ID NO: 15),

AX<sub>3</sub>FXXKX<sub>4</sub>KTXNXWX<sub>5</sub>FX<sub>3</sub>PXK (SEQ ID NO:16),

QXL(I/L)X<sub>2</sub>IX<sub>9</sub>MX<sub>10</sub>PLGKLX<sub>3</sub>QIX<sub>6</sub>L (SEQ ID NO:17),

FYTXIPHXFGX<sub>3</sub>PP (SEQ ID NO:18), and

KX<sub>3</sub>LX<sub>2</sub>LXDIEXAX<sub>2</sub>L (SEQ ID NO:19)

in which the X radicals are, independently of one another, any amino acid.

40. (currently amended) The PARP homolog as claimed in claim 38, **further** comprising sequences:

LX<sub>9</sub>NX<sub>2</sub>YX<sub>2</sub>QLLX(D/E)X<sub>10/11</sub>WGRVG (SEQ ID NO: 15)  
AX<sub>3</sub>FXXKX<sub>4</sub>KTXXNXWX<sub>5</sub>FX<sub>3</sub>PXK (SEQ ID NO:16),  
QXL(I/L)X<sub>2</sub>IX<sub>9</sub>MX<sub>10</sub>PLGKLX<sub>3</sub>QIX<sub>6</sub>L (SEQ ID NO:17),  
FYTXIPHXFGX<sub>3</sub>PP (SEQ ID NO:18), and  
KX<sub>3</sub>LX<sub>2</sub>LXDIEXAX<sub>2</sub>L (SEQ ID NO:19)

in which the X radicals are, independently of one another, any amino acid.

41. (currently amended) The PARP homolog as claimed in claim 38, **further** comprising sequences:

LX<sub>9</sub>NX<sub>2</sub>YX<sub>2</sub>QLLX(D/E)X<sub>10/11</sub>WGRVG (SEQ ID NO: 15)  
AX<sub>3</sub>FXXKX<sub>4</sub>KTXXNXWX<sub>5</sub>FX<sub>3</sub>PXK (SEQ ID NO:16),  
QXL(I/L)X<sub>2</sub>IX<sub>9</sub>MX<sub>10</sub>PLGKLX<sub>3</sub>QIX<sub>6</sub>L (SEQ ID NO:17),  
FYTXIPHXFGX<sub>3</sub>PP (SEQ ID NO:18), and  
KX<sub>3</sub>LX<sub>2</sub>LXDIEXAX<sub>2</sub>L (SEQ ID NO:19)

in which the X radicals are, independently of one another, any amino acid, wherein

LX<sub>9</sub>NX<sub>2</sub>YX<sub>2</sub>QLLX(D/E)X<sub>10/11</sub>WGRVG (SEQ ID NO:15)

is closest to the N terminus.

42. (currently amended) The PARP homolog as claimed in claim 1, **further** comprising sequences:

LX<sub>9</sub>NX<sub>2</sub>YX<sub>2</sub>QLLX(D/E)X<sub>10/11</sub>WGRVG (SEQ ID NO: 15)  
AX<sub>3</sub>FXXKX<sub>4</sub>KTXXNXWX<sub>5</sub>FX<sub>3</sub>PXK (SEQ ID NO:16),  
QXL(I/L)X<sub>2</sub>IX<sub>9</sub>MX<sub>10</sub>PLGKLX<sub>3</sub>QIX<sub>6</sub>L (SEQ ID NO:17),  
FYTXIPHXFGX<sub>3</sub>PP (SEQ ID NO:18), and  
KX<sub>3</sub>LX<sub>2</sub>LXDIEXAX<sub>2</sub>L (SEQ ID NO:19)

in which the X radicals are, independently of one another, any amino acid.

43. (currently amended) The PARP homolog as claimed in claim 1, ~~further~~ comprising sequences:

LX<sub>9</sub>NX<sub>2</sub>YX<sub>2</sub>QLLX(D/E)X<sub>10/11</sub>WGRVG (SEQ ID NO: 15)  
AX<sub>3</sub>FXKX<sub>4</sub>KTXXNWX<sub>5</sub>FX<sub>3</sub>PXK (SEQ ID NO:16),  
QXL(I/L)X<sub>2</sub>IX<sub>9</sub>MX<sub>10</sub>PLGKLX<sub>3</sub>QIX<sub>6</sub>L (SEQ ID NO:17),  
FYTIXIPHXFGX<sub>3</sub>PP (SEQ ID NO:18), and  
KX<sub>3</sub>LX<sub>2</sub>LXDIEAX<sub>2</sub>L (SEQ ID NO:19)

in which the X radicals are, independently of one another, any amino acid, wherein

LX<sub>9</sub>NX<sub>2</sub>YX<sub>2</sub>QLLX(D/E)X<sub>10/11</sub>WGRVG (SEQ ID NO:15)

is closest to the N terminus.

44. (currently amended) The PARP homolog as claimed in claim 1, ~~further~~ comprising at least one of the following:

GX<sub>3</sub>LXEVALG (SEQ ID NO: 20),  
GX<sub>2</sub>SX<sub>4</sub>GX<sub>3</sub>PX<sub>4</sub>LXGX<sub>2</sub>V (SEQ ID NO: 21), and  
E(Y/F)X<sub>2</sub>YXYX<sub>3</sub>QXYLL (SEQ ID NO: 22)

in which a is 7 to 9 and

X is any amino acid.

45. (currently amended) The PARP homolog as claimed in claim 1, ~~further~~ comprising

GX<sub>3</sub>LXEVALG (SEQ ID NO: 20),  
GX<sub>2</sub>SX<sub>4</sub>GX<sub>3</sub>PX<sub>4</sub>LXGX<sub>2</sub>V (SEQ ID NO: 21), and  
E(Y/F)X<sub>2</sub>YX<sub>3</sub>QX<sub>4</sub>YLL (SEQ ID NO: 22)

in which a is 7 to 9 and

X is any amino acid.

46. (currently amended) The PARP homolog as claimed in claim 1, ~~further~~ comprising

GX<sub>3</sub>LXEVALG (SEQ ID NO: 20),  
GX<sub>2</sub>SX<sub>4</sub>GX<sub>3</sub>PX<sub>4</sub>LXGX<sub>2</sub>V (SEQ ID NO: 21), and

E(Y/F)X<sub>2</sub>YX<sub>3</sub>QX<sub>4</sub>YLL (SEQ ID NO: 22)

in which a is 7 to 9 and

X is any amino acid, wherein

E(Y/F)X<sub>2</sub>YX<sub>3</sub>QX<sub>4</sub>YLL (SEQ ID NO: 22)

is closest to the C terminus.

47. (currently amended) An isolated poly(ADP-ribose) polymerase (PARP) homolog comprising human PARP2 (SEQ ID NO: 2) ~~or a functional equivalent thereof which is at least 95% homologous to~~ or a PARP homologue having at least 85% identity with human PARP2 (SEQ ID NO: 2), which exhibits poly(ADP-ribose)-synthesizing activity, and has an amino acid sequence which

- a) has a functional NAD<sup>+</sup> binding domain comprising the sequence

PX<sub>n</sub>(S/T)GX<sub>3</sub>GKGIYFA (SEQ ID NO:11)

in which n is an integral value from 1 to 5, and the X radicals are, independently of one another, any amino acid;

and

- b) lacks a zinc finger sequence.

48. (previously presented) The PARP homolog as claimed in claim 47, wherein said PARP lacks a zinc finger sequence of the formula

CX<sub>2</sub>CX<sub>m</sub>HX<sub>2</sub>C (SEQ ID NO:30)

in which m is an integral value of 28 or 30, and

the X radicals are, independently of one another, any amino acid.

49. (previously presented) The PARP homolog as claimed in claim 47, wherein the functional NAD<sup>+</sup> binding domain comprises the following sequence:

(S/T)XGLR(I/V)XPX<sub>n</sub>(S/T)GX<sub>3</sub>GKGIYFA (SEQ ID NO:12)

in which n is an integral value from 1 to 5, and

the X radicals are, independently of one another, any amino acid.

50. (previously presented) The PARP homolog as claimed in claim 47, wherein the functional NAD<sup>+</sup> binding domain comprises the following sequence:  
LLWHG(S/T)X<sub>7</sub>IL(S/T)XGLR(I/V)XPX<sub>n</sub>(S/T)GX<sub>3</sub>GKGIYFAX<sub>3</sub>SKSAXY (SEQ ID NO:13)  
in which n is an integral value from 1 to 5, and  
the X radicals are, independently of one another, any amino acid.
51. (currently amended) The PARP homolog as claimed in claim 47, further comprising a leucine zipper-like sequence:  
(L/V)X<sub>6</sub>LX<sub>6</sub>LX<sub>6</sub>L (SEQ ID NO: 14)  
wherein X radicals are, independently of one another, any amino acid.
52. (currently amended) The PARP homolog as claimed in claim 51, further comprising at least one of the following sequences:  
LX<sub>9</sub>NX<sub>2</sub>YX<sub>2</sub>QLLX(D/E)X<sub>10/11</sub>WGRVG (SEQ ID NO: 15),  
AX<sub>3</sub>FXX<sub>4</sub>KTXNXWX<sub>5</sub>FX<sub>3</sub>PXX (SEQ ID NO:16),  
QXL(I/L)X<sub>2</sub>IX<sub>9</sub>MX<sub>10</sub>PLGKLX<sub>3</sub>QIX<sub>6</sub>L (SEQ ID NO:17),  
FYTIXIPHXFGX<sub>3</sub>PP (SEQ ID NO:18), and  
KX<sub>3</sub>LX<sub>2</sub>LXDIEXAX<sub>2</sub>L (SEQ ID NO:19)  
in which the X radicals are, independently of one another, any amino acid.
53. (currently amended) The PARP homolog as claimed in claim 51, further comprising:  
LX<sub>9</sub>NX<sub>2</sub>YX<sub>2</sub>QLLX(D/E)X<sub>10/11</sub>WGRVG (SEQ ID NO: 15),  
AX<sub>3</sub>FXX<sub>4</sub>KTXNXWX<sub>5</sub>FX<sub>3</sub>PXX (SEQ ID NO:16),  
QXL(I/L)X<sub>2</sub>IX<sub>9</sub>MX<sub>10</sub>PLGKLX<sub>3</sub>QIX<sub>6</sub>L (SEQ ID NO:17),  
FYTIXIPHXFGX<sub>3</sub>PP (SEQ ID NO:18), and  
KX<sub>3</sub>LX<sub>2</sub>LXDIEXAX<sub>2</sub>L (SEQ ID NO:19)  
in which the X radicals are, independently of one another, any amino acid.

54. (currently amended) The PARP homolog as claimed in claim 51, ~~further~~ comprising:

LX<sub>9</sub>NX<sub>2</sub>YX<sub>2</sub>QLLX(D/E)X<sub>10/11</sub>WGRVG (SEQ ID NO: 15),  
AX<sub>3</sub>FXKX<sub>4</sub>KTXNXWX<sub>5</sub>FX<sub>3</sub>PXK (SEQ ID NO:16),  
QXL(I/L)X<sub>2</sub>IX<sub>9</sub>MX<sub>10</sub>PLGKLX<sub>3</sub>QIX<sub>6</sub>L (SEQ ID NO:17),  
FYTXIPHXFGX<sub>3</sub>PP (SEQ ID NO:18), and  
KX<sub>3</sub>LX<sub>2</sub>LXDIEAX<sub>2</sub>L (SEQ ID NO:19)

in which the X radicals are, independently of one another, any amino acid, wherein

LX<sub>9</sub>NX<sub>2</sub>YX<sub>2</sub>QLLX(D/E)X<sub>10/11</sub>WGRVG (SEQ ID NO: 15)

is closest to the N terminus.

55. (currently amended) The PARP homolog as claimed in claim 47, ~~further~~ comprising at least one of the following:

GX<sub>3</sub>LXEVALG (SEQ ID NO: 20),  
GX<sub>2</sub>SX<sub>4</sub>GX<sub>3</sub>PX<sub>4</sub>LXGX<sub>2</sub>V (SEQ ID NO: 21), and  
E(Y/F)X<sub>2</sub>YX<sub>3</sub>QX<sub>4</sub>YLL (SEQ ID NO: 22)

in which a is 7 to 9 and

X is any amino acid.

56. (currently amended) The PARP homolog as claimed in claim 47, ~~further~~ comprising

GX<sub>3</sub>LXEVALG (SEQ ID NO: 20),  
GX<sub>2</sub>SX<sub>4</sub>GX<sub>3</sub>PX<sub>4</sub>LXGX<sub>2</sub>V (SEQ ID NO: 21), and  
E(Y/F)X<sub>2</sub>YX<sub>3</sub>QX<sub>4</sub>YLL (SEQ ID NO: 22)

in which a is 7 to 9 and

X is any amino acid.

57. (currently amended) The PARP homolog as claimed in claim 47, ~~further~~ comprising

GX<sub>3</sub>LXEVALG (SEQ ID NO: 20),  
GX<sub>2</sub>SX<sub>4</sub>GX<sub>3</sub>PX<sub>4</sub>LXGX<sub>2</sub>V (SEQ ID NO: 21), and



E(Y/F)X<sub>2</sub>YX<sub>3</sub>QX<sub>4</sub>YLL (SEQ ID NO: 22)

in which a is 7 to 9 and

X is any amino acid, wherein

E(Y/F)X<sub>2</sub>YX<sub>3</sub>QX<sub>4</sub>YLL (SEQ ID NO: 22)

is closest to the C terminus.

58. (currently amended) The PARP homolog as claimed in claim 51, ~~further~~ comprising at least one of the following:

GX<sub>3</sub>LXVALG (SEQ ID NO: 20),

GX<sub>2</sub>SX<sub>4</sub>GX<sub>3</sub>PX<sub>a</sub>LXGX<sub>2</sub>V (SEQ ID NO: 21), and

E(Y/F)X<sub>2</sub>YX<sub>3</sub>QX<sub>4</sub>YLL (SEQ ID NO: 22)

in which a is 7 to 9 and

X is any amino acid.

59. (currently amended) The PARP homolog as claimed in claim 51, ~~further~~ comprising

GX<sub>3</sub>LXEVALG (SEQ ID NO: 20),

GX<sub>2</sub>SX<sub>4</sub>GX<sub>3</sub>PX<sub>a</sub>LXGX<sub>2</sub>V (SEQ ID NO: 21), and

E(Y/F)X<sub>2</sub>YX<sub>3</sub>QX<sub>4</sub>YLL (SEQ ID NO: 22)

in which a is 7 to 9 and

X is any amino acid.

60. (currently amended) The PARP homolog as claimed in claim 51, ~~further~~ comprising

GX<sub>3</sub>LXEVALG (SEQ ID NO: 20),

GX<sub>2</sub>SX<sub>4</sub>GX<sub>3</sub>PX<sub>a</sub>LXGX<sub>2</sub>V (SEQ ID NO: 21), and

E(Y/F)X<sub>2</sub>YX<sub>3</sub>QX<sub>4</sub>YLL (SEQ ID NO: 22)

in which a is 7 to 9 and

X is any amino acid, wherein

E(Y/F)X<sub>2</sub>YX<sub>3</sub>QX<sub>4</sub>YLL (SEQ ID NO: 22)

is closest to the C terminus.

Application No.: 09/701,586

Inventor: Kock et al.

Docket No.: 49100

61. (new)      An isolated and purified-poly(ADP-ribose) polymerase (PARP) homolog comprising human PARP2 (SEQ ID NO: 2).